AU 1805

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/711,961

DATE: 12/12/96
TIME: 11:27:31

INPUT SET: S14333.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3   (1)    General Information:
 4   (i) APPLICANT: Arthur A. Branstrom
 5   Donata R. Sizemore
 6   Jerald C. Sadoff
 7
 8   (ii) TITLE OF INVENTION: Bacterial Delivery System
 9
10   (iii) NUMBER OF SEQUENCES:   8
11
12   (iv) CORRESPONDENCE ADDRESS:
13   (A) ADDRESSEE:   John Moran
14   (B) STREET:   USA MRMC -  MCMR-JA
15   (C) CITY: FORT DETRICK, FREDERICK
16   (D) STATE: MARYLAND
17   (E) COUNTRY: USA
18   (F) ZIP: 21702-5012
19
20   (v) COMPUTER READABLE FORM:
21   (A) MEDIUM TYPE: Floppy disk
22   (B) COMPUTER: Apple Macintosh
23   (C) OPERATING SYSTEM: Macintosh 7.5
24   (D) SOFTWARE: Microsoft Word
25
26   (vi) CURRENT APPLICATION DATA:
27   (A) APPLICATION NUMBER:
28   (B) FILING DATE:
29   (C) CLASSIFICATION:
30
31   (vii) PRIOR APPLICATION DATA:
32   (A) APPLICATION NUMBER:
33   (B) FILING DATE:
34
35   (viii) ATTORNEY/AGENT INFORMATION:
36   (A) NAME: Moran, John
37   (B) REGISTRATION NUMBER: 26,313
38   (C) REFERENCE/DOCKET NUMBER:
39
40   (ix) TELECOMMUNICATION INFORMATION
41   (A) TELEPHONE: (301) 619-2065
42   (B) TELEFAX:   (301) 619-7714
43
44   (2) INFORMATION FOR SEQ ID NO:1:
45
46   (i) SEQUENCE CHARACTERISTICS:
```

**RAW SEQUENCE LISTING**
PATENT APPLICATION US/08/711,961

*INPUT SET: S14333.raw*

```
47   (A) LENGTH: 1674 bas  pairs
48   (B) TYPE: Nucleic acid
49   (C) STRANDEDNESS: Double
50   (D) TOPOLOGY: Linear
51
52
53   (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 1:
54   TCCATAATCA  GGATCAATAA  AACTGCTGCA  GAAATGATTT     40
55   CATTCATAAC  TCAAATTCCC  TGATAATTGC  CGCGGACTTT     80
56   CTGCGTGCTA  ACAAAGCAGG  ATAAGTCGCA  TTACTCATGG    120
57   CTTCGCTATC  ATTGATTAAT  TTCACTTGCG  ACTTTGGCTG    160
58   CTTTTTGTAT  GGTGAAAGAT  GTGCCAAGAG  GAGACCGGCA    200
59   CATTTATACA  GCACACATCT  TTGCAGGAAA  AAAACGCTTA    240
60   TGAAAAATGT  TGGTTTTATC  GGCTGGCGCG  GTATGGTCGG    280
61   CTCCGTTCTC  ATGCAACGCA  TGGTTGAAGA  GCGCGACTTC    320
62   GACGCCATTC  GCCCTGTCTT  CTTTTCTACT  TCTCAGCTTG    360
63   GCCAGGCTGC  GCCGTCTTTT  GGCGGAACCA  CTGGCACACT    400
64   TCAGGATGCC  TTTGATCTGG  AGGCGCTAAA  GGCCCTCGAT    440
65   ATCATTGTGA  CCTGTCAGGG  CGGCGATTAT  ACCAACGAAA    480
66   TCTATCCAAA  GCTTCGTGAA  AGCGGATGGC  AAGGTTACTG    520
67   GATTGACGCA  GCATCGTCTC  TGCGCATGAA  AGATGACGCC    560
68   ATCATCATTC  TTGACCCCGT  CAATCAGGAC  GTCATTACCG    600
69   ACGGATTAAA  TAATGGCATC  AGGACTTTTG  TTGGCGGTAA    640
70   CTGTACCGTA  AGCCTGATGT  TGATGTCGTT  GGGTGGTTTA    680
71   TTCGCCAATG  ATCTTGTTGA  TTGGGTGTCC  GTTGCAACCT    720
72   ACCAGGCCGC  TTCCGGCGGT  GGTGCGCGAC  ATATGCGTGA    760
73   GTTATTAACC  CAGATGGGCC  ATCTGTATGG  CCATGTGGCA    800
74   GATGAACTCG  CGACCCCGTC  CTCTGCTATT  CTCGATATCG    840
75   AACGCAAAGT  CACAACCTTA  ACCCGTAGCG  GTGAGCTGCC    880
76   GGTGGATAAC  TTTGGCGTGC  CGCTGGCGGG  TAGCCTGATT    920
77   CCGTGGATCG  ACAAACAGCT  CGATAACGGT  CAGAGCCGCG    960
78   AAGAGTGGAA  AGGGCAGGCG  GAAACCAACA  AGATCCTCAA   1000
79   CACATCTTCC  GTAATTCCGG  TAGATGGTTT  ATGTGTGCGT   1040
80   GTCGGGGCAT  TGCGCTGCCA  CAGCCAGGCA  TTCACTATTA   1080
81   AATTGAAAAA  AGATGTGTCT  ATTCCGACCG  TGGAAGAACT   1120
82   GCTGGCTGCG  CACAATCCGT  GGGCGAAAGT  CGTTCCGAAC   1160
83   GATCGGGAAA  TCACTATGCG  TGAGCTAACC  CCAGCTGCCG   1200
84   TTACCGGCAC  GCTGACCACG  CCGGTAGGCC  GCCTGCGTAA   1240
85   GCTGAATATG  GGACCAGAGT  TCCTGTCAGC  CTTTACCGTG   1280
86   GGCGACCAGC  TGCTGTGGGG  GGCCGCGGAG  CCGCTGCGTC   1320
87   GGATGCTTCG  TCAACTGGCG  TAATCTTTAT  TCATTAAATC   1360
88   TGGGGCGCGA  TGCCGCCCCT  GTTAGTGCGT  AATACAGGAG   1400
89   TAAGCGCAGA  TGTTTCATGA  TTTACCGGGA  GTTAAATAGA   1440
90   GCATTGGCTA  TTCTTTAAGG  GTGGCTGAAT  ACATGAGTAT   1480
91   TCACAGCCTT  ACCTGAAGTG  AGGACGACGC  AGAGAGGATG   1520
92   CACAGAGTGC  TGCGCCGTTC  AGGTCAAAAA  AATGTCACAA   1560
93   CCAGAAGTCA  AAAATCCAAT  TGGATGGGGT  GACACAATAA   1600
94   AACAGGAAGA  CAAGCATGTC  CGATCGTATC  GATAGAGACG   1640
95   TGATTAACGC  GCTAATTGCA  GGCCATTTTG  CGGA         1674
96
97   (2) INFORMATION FOR SEQ ID NO:2:
98
99   (i) SEQUENCE CHARACTERISTICS:
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```
100   (A) LENGTH: 1121 base pairs
101   (B) TYPE: Nucleic acid
102   (C) STRANDEDNESS: Double
103   (D) TOPOLOGY: Linear
104   (ii) MOLECULE TYPE: Other nucleic acid
105   (A) DESCRIPTION: The E. coli asd gene coding for b-aspartic semialdehyde dehydrogen
106
107   (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 2:
108
109   TCCATAATCA  GGATCAATAA  AACTGCTGCA  GAAATGATTT      40
110   CATTCATAAC  TCAAATTCCC  TGATAATTGC  CGCGGACTTT      80
111   CTGCGTGCTA  ACAAAGCAGG  ATAAGTCGCA  TTACTCATGG     120
112   CTTCGCTATC  ATTGATTAAT  TTCACTTGCG  ACTTTGGCTG     160
113   CTTTTTGTAT  GGTGAAAGAT  GTGCCAAGAG  GAGACCGGCA     200
114   CATTTATACA  GCACACATCT  TTGCAGGAAA  AAAACGCTTA     240
115   TGAAAAATGT  TGGTTTTATC  GGCTGGCGCG  GTATGGTCGG     280
116   CTCCGTTCTC  ATGCAACGCA  TGGTTGAAGA  GCGCGACTTC     320
117   GACGCCATTC  GCCCTGTCTT  CTTTTCTACT  TCTCAGCTTG     360
118   GCCAGGCTGC  GCCGTCTTTT  GGCGGAACCA  CTGGCACACT     400
119   TCAGGATGCC  TTTGATCTGG  AGGCGCTAAA  GGCCCTCGGA     440
120   TCCTCAACAC  ATCTTCCGTA  ATTCCGGTAG  ATGGTTTATG     480
121   TGTGCGTGTC  GGGGCATTGC  GCTGCCACAG  CCAGGCATTC     520
122   ACTATTAAAT  TGAAAAAAGA  TGTGTCTATT  CCGACCGTGG     560
123   AAGAACTGCT  GGCTGCGCAC  AATCCGTGGG  CGAAAGTCGT     600
124   TCCGAACGAT  CGGGAAATCA  CTATGCGTGA  GCTAACCCCA     640
125   GCTGCCGTTA  CCGGCACGCT  GACCACGCCG  GTAGGCCGCC     680
126   TGCGTAAGCT  GAATATGGGA  CCAGAGTTCC  TGTCAGCCTT     720
127   TACCGTGGGC  GACCAGCTGC  TGTGGGGGGC  CGCGGAGCCG     760
128   CTGCGTCGGA  TGCTTCGTCA  ACTGGCGTAA  TCTTTATTCA     800
129   TTAAATCTGG  GGCGCGATGC  CGCCCCTGTT  AGTGCGTAAT     840
130   ACAGGAGTAA  GCGCAGATGT  TTCATGATTT  ACCGGGAGTT     880
131   AAATAGAGCA  TTGGCTATTC  TTTAAGGGTG  GCTGAATACA     920
132   TGAGTATTCA  CAGCCTTACC  TGAAGTGAGG  ACGACGCAGA     960
133   GAGGATGCAC  AGAGTGCTGC  GCCGTTCAGG  TCAAAAAAT    1000
134   GTCACAACCA  GAAGTCAAAA  ATCCAATTGG  ATGGGGTGAC   1040
135   ACAATAAAAC  AGGAAGACAA  GCATGTCCGA  TCGTATCGAT   1080
136   AGAGACGTGA  TTAACGCGCT  AATTGCAGGC  CATTTTGCGG   1120
137   A                                               1121
138
139   (2) INFORMATION FOR SEQ ID NO:3:
140
141   (i) SEQUENCE CHARACTERISTICS:
142   (A) LENGTH: 22 base pairs
143   (B) TYPE: Nucleic acid
144   (C) STRANDEDNESS: Double
145   (D) TOPOLOGY: Linear
146
147   (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 3:
148
149   AGATCTCCCT  GATAATTGCC  GC                 22
150
151
152
```

153    (2) INFORMATION FOR SEQ ID NO:4:
154
155    (i) SEQUENCE CHARACTERISTICS:
156    (A) LENGTH: 26 base pairs
157    (B) TYPE: Nucleic acid
158    (C) STRANDEDNESS: Double
159    (D) TOPOLOGY: Linear
160
161
162    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 4:
163
164    AGATCTCGCT  TACTCCTGTA  TTACGC          26
165
166
167    (2) INFORMATION FOR SEQ ID NO:5:
168
169    (i) SEQUENCE CHARACTERISTICS:
170    (A) LENGTH: 20 base pairs
171    (B) TYPE: Nucleic acid
172    (C) STRANDEDNESS: Double
173    (D) TOPOLOGY: Linear
174
175
176    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 5:
177
178    CGAGGGCCTT  TAGCGCCTCC                          20
179
180
181    (2) INFORMATION FOR SEQ ID NO:6:
182
183    (i) SEQUENCE CHARACTERISTICS:
184    (A) LENGTH: 20 base pairs
185    (B) TYPE: Nucleic acid
186    (C) STRANDEDNESS: Double
187    (D) TOPOLOGY: Linear
188
189
190
191    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 6:
192
193    GATCCTCAAC  ACATCTTCCG                          20
194
195
196    (2) INFORMATION FOR SEQ ID NO:7:
197
198    (i) SEQUENCE CHARACTERISTICS:
199    (A) LENGTH: 22 base pairs
200    (B) TYPE: Nucleic acid
201    (C) STRANDEDNESS: Double
202    (D) TOPOLOGY: Linear
203
204
205    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 7:

```
206
207    GAGCTCCCCT   GATAATTGCC   GC                     22
208
209
210    (2) INFORMATION FOR SEQ ID NO:8:
211
212    (i) SEQUENCE CHARACTERISTICS:
213    (A) LENGTH: 26 base pairs
214    (B) TYPE: Nucleic acid
215    (C) STRANDEDNESS: Double
216    (D) TOPOLOGY: Linear
217
218
219    (xi) SEQUENCE DESCRIPTION:   SEQ ID NO: 8:
220
221    GTCGACCGCT   TACTCCTGTA   TTACGC          26
222
223
224
```

# SEQUENCE VERIFICATION REPORT
## PATENT APPLICATION   US/08/711,961

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